

(FILE 'HOME' ENTERED AT 13:33:32 ON 16 OCT 2000)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, LIFESCI, SCISEARCH, TOXLINE, CABA, BIOTECOM, CANCERLIT, ESHIOBASE' ENTERED AT 13:33:43 ON 16 OCT 2000

L1 4033 S IMPDH OR ((INOSINE (W) MONOPHOSPHATE (W) DEHYDROGENASE?) OR (1
L2 24 S PYGENES AND L1
L3 31 S L1 AND ((STREPTOCOCC? OR PYGENES)
L4 7 DUP REM L3 (24 DUPLICATES REMOVED)
L5 66589 S (THREE (W) DIMENSIONAL (W) STRUCTURE?) OR (3D (W) STRUCTURE?) O
L6 0 S L1 AND L2 AND L5
L7 13789 S L5 AND ((CRYSTAL OR X-RAY OR (X(W) RAY)) (3W) STRUCTURE?)
L8 18 S L1 AND L3 AND ((CRYSTAL OR X-RAY OR (X(W) RAY)) (3W) STRUCTU
L9 3 DUP REM L8 (15 DUPLICATES REMOVED)
L10 0 S L4 AND L7
L11 3 S L4 AND ((CRYSTAL OR X-RAY OR (X(W) RAY)) (3W) STRUCTURE?)
L12 3 DUP REM L11 (10 DUPLICATES REMOVED)

L4 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2000 ACS
AN 1999:464100 CAPLUS

TI Method to identify specific inhibitors of ***inosine***
monophosphate* **dehydrogenase*** (***IMPDH***)
IN Collarty, Frank R.; Huberman, Eliezer
PA The University of Chicago, USA
SO PCT Int. Appl., 34 pp.
DT Patent
LA English
FAN CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

PI WO 9933996 A1 19990708 WO 1998-182109 19981223
W: AL, AM, AT, AU, AZ, BA, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
DK, EE, ES, FI, GB, GD, GE, GH, GM, GR, HU, ID, IL, IN, IS, JP,
KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, BG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, IS, MM, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9915022 A1 19990719 AU 1999-15022 19981223

PRAI US 1997-99758 19971224
MO 1998-182109 19981223

AB This invention relates to methods to identify specific inhibitors of the
purine nucleotide synthesis enzyme, ***IMPDH***. ***IMPDH*** is
an essential enzyme found in all free-living organisms from humans to
bacteria and is an important therapeutic target. The invention allows the
identification of specific inhibitors of any ***IMPDH*** enzyme which
can be expressed in a functional form in a recombinant host cell. To
illustrate the utility of the invention, the coding sequence of human and
Streptococcus, ***pyogenes***, ***IMPDH*** were cloned into
the pJF18H expression vector. A variety of eukaryotic or prokaryotic
host systems commonly used for the expression. prodn. Utilization
of exogenous guanosine as a control component of the methods allows for
the identification of inhibitors specific for ***IMPDH*** rather than
other causes of decreased cell proliferation.

L4 ANSWER 2 OF 7 MEDLINE DUPLICATE 1
TI Characteristics and crystal structure of bacterial inosine-5'-
monophosphate dehydrogenase.

AU Zhang R; Evans G; Rotella F J; Westbrook E M; Beno D; Huberman E;
SO BIOCHEMISTRY, (1999 Apr 13) 38 (15) 4691-700.
Journal code: A06. ISSN: 0006-2960.

AB ***IMP*** **dehydrogenase*** (***IMPDH***) is an essential
enzyme that catalyzes the first step unique to GTP synthesis. To provide a
basis for the evaluation of ***IMPDH*** inhibitors as antimicrobial
agents, we have expressed and characterized ***IMPDH*** from the
pathogenic bacterium ***Streptococcus***. ***pyogenes***. Our
results show that the biochemical and kinetic characteristics of S.
pyogenes are similar to other bacterial
IMPDH enzymes. However, the lack of sensitivity to mycophenolic
acid and the Km for NAD (1180-microm) exemplify some of the differences
between the bacterial and mammalian ***IMPDH*** enzymes, making it an
attractive target for antimicrobial agents. To evaluate the basis for
these differences, we determined the crystal. obtained with
synchrotron radiation from the undulator beamline (19ID) of the Structural
Biology Center at Argonne's Advanced Photon Source. S. ***pyogenes***

IMPDH is a tetramer with its four subunits related by a
crystallographic 4-fold axis. The protein is composed of two domains:
flap as an essential catalytic element and indicate there are
significant differences in the catalytic environment of bacterial and
mammalian ***IMPDH*** enzymes. Comparison of the structure of
bacterial ***IMPDH*** with the known partial structures from
eukaryotic organisms will provide an explanation of their distinct
properties and contribute to the design of specific bacterial
IMPDH inhibitors

L4 ANSWER 3 OF 7 MEDLINE DUPLICATE 2
TI ***IMP*** **dehydrogenase*** : mechanism of action and inhibition.
AU Hedstrom L
SO CURRENT MEDICINAL CHEMISTRY, (1999 Jul) 6 (7) 545-60. Ref: 89
Journal code: C02. ISSN: 0929-8673.

AB ***IMP*** **dehydrogenase*** : mechanism of action and inhibition.
inosine **monophosphate*** **dehydrogenase*** (***IMPDH***)
catalyzes the conversion of IMP to XMP with the concomitant
reduction of NAD to NADH. This reaction is the rate-limiting step in
guanine nucleotide biosynthesis. ***IMPDH*** is a proven target for
immunosuppressive, anticancer and antiviral chemotherapy, and may also be
a target for antimicrobial agents. ***IMPDH*** is activated by
monovalent cations, and one monovalent cation binding site appears to have
been identified. The mechanism of ***IMPDH*** involves formation and
hydrolysis of a covalent enzyme intermediate (E-XMP*) in a reaction
reminiscent of glyceraldehyde-3-phosphate dehydrogenase. Substrates bind
to ***IMPDH*** in a random order, hydride transfer is fast and NADH
release precedes hydrolysis of E-XMP*. The hydrolysis of E-XMP* is.

L4 ANSWER 4 OF 7 MEDLINE DUPLICATE 3
TI Differential signatures of bacterial and mammalian ***IMP***
dehydrogenase enzymes.
AU Zhang R; Evans G; Rotella F; Westbrook E; Huberman E; Joachimiak A;
SO Collarty F R
CURRENT MEDICINAL CHEMISTRY, (1999 Jul) 6 (7) 537-43.
Journal code: C02. ISSN: 0929-8673.
Differential signatures of bacterial and mammalian ***IMP***
dehydrogenase enzymes.

AB ***IMP*** dehydrogenase*** (***IMP***) is an essential enzyme of de novo guanine nucleotide synthesis. ***IMP*** inhibitors have clinical utility as antiviral, anticancer or immunosuppressive agents. The essential nature of this enzyme suggests its therapeutic applications may be extended to the development of antimicrobial agents. Bacterial ***IMP*** enzymes show biochemical and kinetic characteristics that are different than the mammalian ***IMP*** enzymes, suggesting ***IMP*** may be an attractive target for the development of antimicrobial agents. We suggest that the biochemical and kinetic differences between . . . is a prerequisite for the rational identification of agents that specifically target the bacterial enzyme. We used sequence alignments of ***IMP*** proteins to identify sequence signatures associated with bacterial or eukaryotic ***IMP*** enzymes. These selections were further refined to discern those likely to have a role in catalysis using information derived from the bacterial and mammalian ***IMP*** crystal structures and site-specific mutagenesis. Candidate bacterial sequence signatures identified by this process include regions involved in subunit interactions, the . . . a secondary pattern of amino acid conservation associated with the major phylogenetic groups. Elucidation of the basis for this mammalian/bacterial ***IMP*** signature will provide insight into the catalytic mechanism of this enzyme and the foundation for the development of highly specific.

L4 ANSWER 5 OF 7 MEDLINE DUPLICATE 4
TI ***IMP*** dehydrogenase*** : structural aspects of inhibitor binding.
AU Goldstein B M; Colby T D
SO CURRENT MEDICINAL CHEMISTRY, (1999 JUL) 6 (7) 519-36. Ref: 118
Journal code: C02. ISSN: 0929-8673.
TI ***IMP*** dehydrogenase*** : structural aspects of inhibitor binding.

AB ***IMP*** dehydrogenase*** (***IMP***) is an essential enzyme of de novo guanine nucleotide synthesis. ***IMP*** inhibitors have clinical utility as antiviral, anticancer or immunosuppressive agents. The essential nature of this enzyme suggests its therapeutic applications may be extended to the development of antimicrobial agents. Bacterial ***IMP*** enzymes show biochemical and kinetic characteristics that are different than the mammalian ***IMP*** enzymes, suggesting ***IMP*** may be an attractive target for the development of antimicrobial agents. We suggest that the biochemical and kinetic differences between . . . is a prerequisite for the rational identification of agents that specifically target the bacterial enzyme. We used sequence alignments of ***IMP*** proteins to identify sequence signatures associated with bacterial or eukaryotic ***IMP*** enzymes. These selections were further refined to discern those likely to have a role in catalysis using information derived from the bacterial and mammalian ***IMP*** crystal structures and site-specific mutagenesis. Candidate bacterial sequence signatures identified by this process include regions involved in subunit interactions, the . . . a secondary pattern of amino acid conservation associated with the major phylogenetic groups. Elucidation of the basis for this mammalian/bacterial ***IMP*** signature will provide insight into the catalytic mechanism of this enzyme and the foundation for the development of highly specific.

L4 ANSWER 6 OF 7 MEDLINE DUPLICATE 5
TI Cloning, sequence analysis and expression of the group A ***streptococcal*** guab gene encoding ***inosine***
monophosphate dehydrogenase***
AU Ashbaugh C D; Wessels M R
SO GENE, (1995 Nov 7) 165 (1) 57-60.
Journal code: F0P. ISSN: 0378-1119.
TI Cloning, sequence analysis and expression of the group A ***streptococcal*** guab gene encoding ***inosine***

AB ***monophosphate*** dehydrogenase*** (***IMP***) is an essential enzyme in the biosynthesis of purines. We cloned a group A ***streptococcal*** (GAS) DNA fragment containing an open reading frame similar to other bacterial guab genes encoding a protein of 493 amino acids. Expression of the GAS guab in an Escherichia coli guab mutant restored ***IMP*** activity, confirming the function of the gene product and demonstrating that the GAS enzyme is active in a heterologous bacterial.

L4 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2000 ACS
TI A simple method for the rapid determination of the stereospecificity of NAD-dependent dehydrogenases applied to mammalian ***IMP***
dehydrogenase and bacterial NADH peroxidase
AU Cooney, David; Hamel, Ernest; Cohen, Marvin; Kang, Gil J.; Datal, Maha; Marquez, Victor
SO Biochim. Biophys. Acta, (1987), 916(1), 89-93
CODEN: BBAQAO; ISSN: 0006-3002
A simple method for the rapid determination of the stereospecificity of NAD-dependent dehydrogenases applied to mammalian ***IMP***
dehydrogenase and bacterial NADH peroxidase.

AB The stereospecificity of ***IMP*** dehydrogenase*** (EC 1.1.1.205) from 2 different sources was determined. The enzyme preps. were obtained from murine lymphoblasts and from Escherichia coli. . . the enzyme from 2 very different species. In addn., the studies described here demonstrated that a/c. dehydrogenase and NADH peroxidase (***Streptococcus*** faecalis), used as auxiliary enzymes, in combination with a microdistr. procedure, may rapidly det. the stereospecificity of any NAD-dependent dehydrogenase.

L9 ANSWER 1 OF 3 MEDLINE DUPLICATE 1
AN 1999218077 MEDLINE
DN 99218077
TI Characteristics and ***crystal*** structure*** of bacterial inosine-5'-monophosphate dehydrogenase.
AU Zhang R; Evans G; Rotella F J; Westbrook E M; Beno D; Huberman E; Joachimiak A; Collart F R
CS Center for Mechanistic Biology and Biotechnology, Argonne National Laboratory, 9700 South Cass Avenue, Argonne, Illinois 60439-4833, USA.
SO BIOCHEMISTRY, (1999 Apr 13) 38 (15) 4691-700.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS PDB-12FJ
EM 199907
L9 ANSWER 2 OF 3 MEDLINE DUPLICATE 2
AN 1999322361 MEDLINE
DN 99322361
TI Differential signatures of bacterial and mammalian ***IMP*** dehydrogenase*** enzymes.
AU Zhang R; Evans G; Rotella F; Westbrook E; Huberman E; Joachimiak A; Collart F R

CS Biosciences Division, Argonne National Laboratory.
 SO CURRENT MEDICAL CHEMISTRY, (1999 Jul) 6 (7) 537-43.
 CY Journal code: C02. ISSN: 0929-8673.
 DT Netherlands
 LA Journal: Article; (JOURNAL ARTICLE)
 FS English
 EM Priority Journals
 EM 199912
 EM 19991203

L9 ANSWER 3 OF 3 MEDLINE
 AN 1999322380 MEDLINE
 DN 99322380
 TI ***IMP*** dehydrogenase*** : structural aspects of inhibitor binding.

AU Goldstein B M; Colby T D
 CS Department of Biochemistry and Biophysics, University of Rochester Medical Center, Rochester, NY, 14642, USA. barry_goldstein@umc.rochester.edu
 SO CURRENT MEDICAL CHEMISTRY, (1999 Jul) 6 (7) 519-36. Ref: 118
 CY Netherlands
 DT Journal: Article; (JOURNAL ARTICLE)
 LA General Review; (REVIEW)
 FS (REVIEW, ACADEMIC)
 EM English
 EM Priority Journals
 EM 199912
 EM 19991203

=> d 1 14

L4 ANSWER 1 OF 7 CAPLUS. COPYRIGHT 2000 ACS
 AN 1999:464100 CAPLUS
 DN 131:83979
 TI Method to identify specific inhibitors of inosine
 IN ***monophosphate*** dehydrogenase*** (***IMPDH***)
 PA Collart, Frank R.; Huberman, Eliezer
 SO The University of Chicago, USA
 SO PCT Int. Appl., 34 pp.
 DT Patent
 LA English
 EM PATENT NO. 1

KIND	DATE	APPLICATION NO.	DATE
PI	WO 9933996	A1 19990708	WO 1998-1B2109 19981223
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, GR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MM, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, BG, CH, CY, DE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SJ, BF, BJ, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
AU	9915022	A1 19990719	AU 1999-15022 19981223
PRAI	US 1997-99758		19971224
WO	1998-1B2109		19981223

RE.CNT 5
 RE
 (1) American Cyanamid Co: EP 0608722 A 1994
 (2) Balzarini And De Clercq: BIOCHEMICAL JOURNAL 1992, V287, P785
 (3) Carr: JOURNAL OF BIOLOGICAL CHEMISTRY 1993, V268(36), P27286 CAPLUS
 (4) Pankiewicz: PHARMACOLOGY AND THERAPEUTICS 1997, V76(1-3), P89 CAPLUS
 (5) Vertex Pharma: WO 9741211 A 1997

=> d kwic 1

L9 ANSWER 1 OF 3 MEDLINE
 TI Characteristics and inosine-5'-monophosphate dehydrogenase. ***IMP*** dehydrogenase*** (***IMPDH***) is an essential enzyme that catalyzes the first step unique to GTP synthesis. To provide a basis for the evaluation of ***IMPDH*** inhibitors as antimicrobial agents, we have expressed and characterized ***IMPDH*** from the pathogenic bacterium ***Streptococcus*** pyogenes***. Our results show that the biochemical and kinetic characteristics of S. ***pyogenes*** are similar to other bacterial ***IMPDH*** enzymes. However, the lack of sensitivity to mycophenolic acid and the Km for NAD (1180 micromol) exemplify some of the differences between the bacterial and mammalian ***IMPDH*** enzymes, making it an attractive target for antimicrobial agents. To evaluate the basis for these differences, we determined the ***crystal*** structure*** of the bacterial enzyme at 1.9 Å with substrate bound in the catalytic site. The structure was determined using selenomethionine-substituted. obtained with synchrotron radiation from the undulator beamline (191D) of the Structural Biology Center at Argonne's Advanced Photon Source. S. ***pyogenes*** ***IMPDH*** is a tetramer with its four subunits related by a crystallographic 4-fold axis. The protein is composed of two domains: . . . and a cytosolic beta-synthase (CBS) dimer domain of so far unknown function. Using information provided by sequence alignments and the ***crystal*** structure***, we prepared several site-specific mutants to examine the role of various active site regions in catalysis. These variants implicate the . . . flap as an essential catalytic element and indicate there are significant differences in the catalytic environment of bacterial and mammalian ***IMPDH*** enzymes. Comparison of the structure of bacterial ***IMPDH*** with the known partial structures from eukaryotic organisms will provide an explanation of their distinct properties and contribute to the design of specific bacterial ***IMPDH*** inhibitors.
 Check Tags: Support, U.S. Gov't, Non-P.H.S.
 Catalytic Domain
 Crystallography, X-Ray
 Dimerization
 Enzyme Inhibitors: PD, pharmacology
 IMP Dehydrogenase: CH, chemistry
 IMP Dehydrogenase: GE, genetics
 IMP Dehydrogenase: ME, metabolism
 Models, Molecular
 Mutagenesis, Site-Directed
 Protein Conformation
 Recombinant Proteins: CH, chemistry
 Recombinant Proteins: GE, genetics
 Recombinant Proteins: ME, metabolism
 Streptococcus pyogenes: EN, enzymology

CT

CN EC 1.1.1.205 (***IMP*** **dehydrogenase***); 0 (Enzyme Inhibitors); 0 (Recombinant Proteins)
 => d kwic 1 14
 L4 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2000 ACS
 TI Method to identify specific inhibitors of (***IMPDH***)
 AB ***monophosphate*** **dehydrogenase***
 This invention relates to methods to identify specific inhibitors of the
 purine nucleotide synthesis enzyme, ***IMPDH*** **IMPDPH*** is
 an essential enzyme found in all free-living organisms from humans to
 bacteria and is an important therapeutic target. The invention allows the
 identification of specific inhibitors of any ***IMPDPH*** enzyme which
 can be expressed in a functional form in a recombinant host cell. To
 illustrate the utility of the invention, the coding sequence of human and
 Streptococcus **Pyogenes*** were cloned into
 the pU118H expression vector. A variety of eukaryotic or prokaryotic
 host systems commonly used for the expression. prodn. Utilization
 of exogenous guanosine as a control component of the methods allows for
 the identification of inhibitors specific for ***IMPDPH*** rather than
 other causes of decreased cell proliferation.
 ST Inhibitor ***Inosine*** **monophosphate*** **dehydrogenase***
 human
 IT Escherichia coli
 (H712, expression host; method to identify specific inhibitors of
 Inosine **monophosphate*** **dehydrogenase***
 IMPDPH)
 IT ***Streptococcus*** **Pyogenes***
 (IMP-encoding gene from; method to identify specific inhibitors of
 Inosine **monophosphate*** **dehydrogenase***
 IMPDPH)
 IT Bacillus subtilis
 Bacteria (Eubacteria)
 Eukaryote (Eukaryotae)
 Insect (Insecta)
 Neurospora
 (expression host; method to identify specific inhibitors of
 Inosine **monophosphate*** **dehydrogenase***
 IMPDPH)
 IT Drug screening
 Molecular cloning
 (method to identify specific inhibitors of ***Inosine***
 monophosphate **dehydrogenase***
 IMPDPH)
 IT Drosophila
 (serani; method to identify specific inhibitors of ***Inosine***
 monophosphate **dehydrogenase***
 IMPDPH)
 IT 118-00-3, Guanosine, biological studies
 RI: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical
 study); BIOL (Biological study)
 (as a control component; method to identify specific inhibitors of
 Inosine **monophosphate*** **dehydrogenase***
 IMPDPH)
 IT 9028-93-7, ***Inosine*** **monophosphate*** **dehydrogenase***
 RI: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (method to identify specific inhibitors of ***Inosine***
 monophosphate **dehydrogenase***
 IMPDPH)

IT 367-93-1
 RI: BUU (Biological use, unclassified); BIOL (Biological study); USES
 (Uses)
 (method to identify specific inhibitors of ***Inosine***
 monophosphate **dehydrogenase***
 IMPDPH)
 => d hist
 (FILE 'HOME' ENTERED AT 13:33:32 ON 16 OCT 2000)
 FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, LIFESCI, SCISEARCH, TOXLINE, CABA,
 BIOTECHNO, CANCERLIT, ESIIOBASE' ENTERED AT 13:33:43 ON 16 OCT 2000
 L1 4033 S IMPDH OR (INOSINE (W) MONOPHOSPHATE (W) DEHYDROGENASE?) OR (I
 L2 24 S PYOGENES AND L1
 L3 31 S L1 AND (STREPTOCOCC? OR PYOGENES)
 L4 7 DUP REM L3 (24 DUPLICATES REMOVED)
 L5 66589 S (THREE (W) DIMENSIONAL (W) STRUCTUR?) OR (3D (W) STRUCTUR?) O
 L6 0 S L1 AND L2 AND L5
 L7 13789 S L5 AND ((CRYSTAL OR X-RAY OR (X(W)RAY)) (3W) STRUCTUR?)
 L8 18 S L1 AND L3 AND ((CRYSTAL OR X-RAY OR (X(W)RAY)) (3W) STRUCTU
 L9 3 DUP REM L8 (15 DUPLICATES REMOVED)
 => s 14 and 117
 <-----User Break----->
 U
 SEARCH ENDED BY USER
 => s 14 and 117
 L10 0 L4 AND L7
 => s 14 and ((crystal or x-ray or (x(w)ray)) (3w) structur?)
 3 FILES SEARCHED...
 9 FILES SEARCHED...
 L11 3 L4 AND ((CRYSTAL OR X-RAY OR (X(W)RAY)) (3W) STRUCTUR?)
 => dup rem 111
 PROCESSING COMPLETED FOR L11
 L12 3 DUP REM L11 (0 DUPLICATES REMOVED)
 => d 1-3
 L12 ANSWER 1 OF 3 MEDLINE
 AN 1999218077 MEDLINE
 DN 99218077
 TI Characteristics and ***crystal*** **structure*** of bacterial
 inosine-5'-monophosphate dehydrogenase.
 AU Zhang R; Evans G; Rotella F J; Westbrook E M; Beno D; Huberman E;
 Joachimiak A; Collart F R
 CS Center for Mechanistic Biology and Biotechnology, Argonne National
 Laboratory, 9700 South Cass Avenue, Argonne, Illinois 60439-6833, USA.
 SO Fcolliat@enl.gov
 BIOCHEMISTRY, (1999 Apr 13) 38 (15) 4691-700.
 Journal code: AOG. ISSN: 0006-2960.

